

The file contains raw read counts for the 10 species examined in the paper:

Species	Assembly used for mapping	Included samples
<i>P. dumerilii</i>	Pdum_transcriptome_v1 (<i>de novo</i> - NCBI BioProject PRJNA271451)	80
<i>S. polychroa</i>	Spol_transcriptome_v1 (<i>de novo</i> - NCBI BioProject PRJNA271420)	58
<i>C. elegans</i>	WS230 (WormBase)	81
<i>H. dujardini</i>	Hduj_transcriptome_v1 (<i>de novo</i> - NCBI BioProject PRJNA271450)	62
<i>D. melanogaster</i>	BDGP5 (Ensembl)	77
<i>S. purpuratus</i>	WHL22 transcriptome ^{2,3}	57
<i>D. rerio</i>	Zv9 (Ensembl)	88
<i>N. vectensis</i>	NvT1 (Stellabae) ⁴	83
<i>A. queenslandica</i>	Aqu2.1 ⁵	51
<i>M. leidyi</i>	MIScaffold09 ^{6,7}	53

For each species there are two sheets:

1. A list of sample IDs and their annotated developmental time
2. The expression matrix including sample IDs, gene names (including ERCC control RNA) and read counts.

REFERENCES

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